

--- QUAD STATS ---

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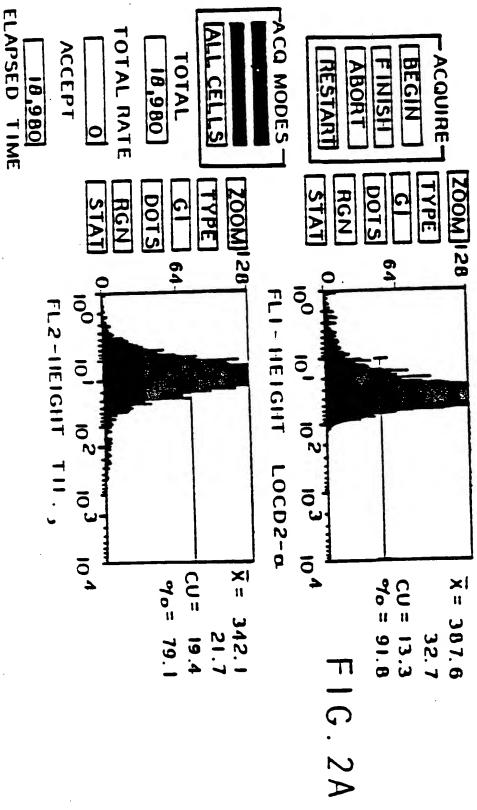
DATE: 9/24/92 GATE G1-R1

PARMETER : FLI - H \ (LOG) FL2-H(LOG) QUAD LOCATION: 17.15 9

#12:/23/CD2019

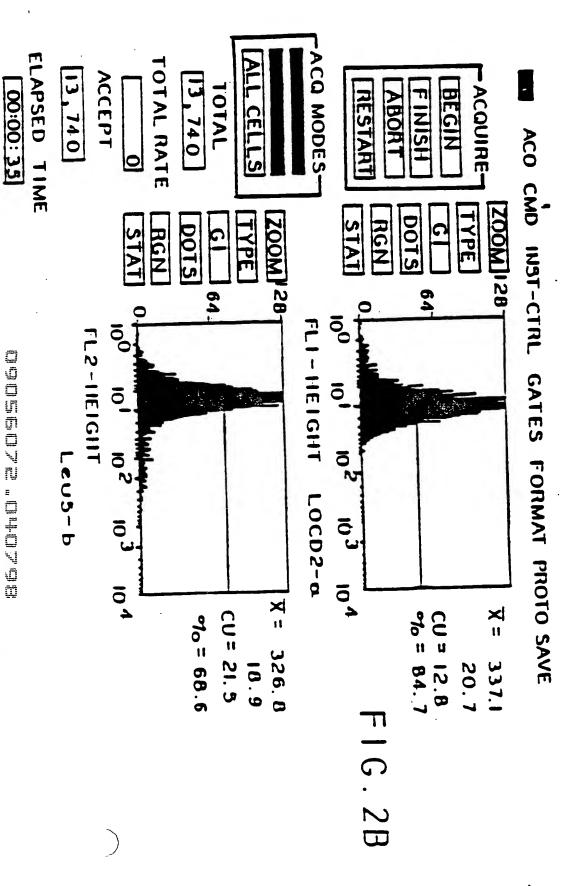
TOTAL=	5000 EVENTS	GATED =	1290 70TOTAL	X MEAN	Y MEAN
IUL	299	23.18	3.98	11.41	<i>2</i> 84.69
2UR	851	65.97	17.02	32.70	630.65
3LL	135	10.47	2.70	4.08	3 .31
4LR	5	0.39	0.10	25.11	6.54





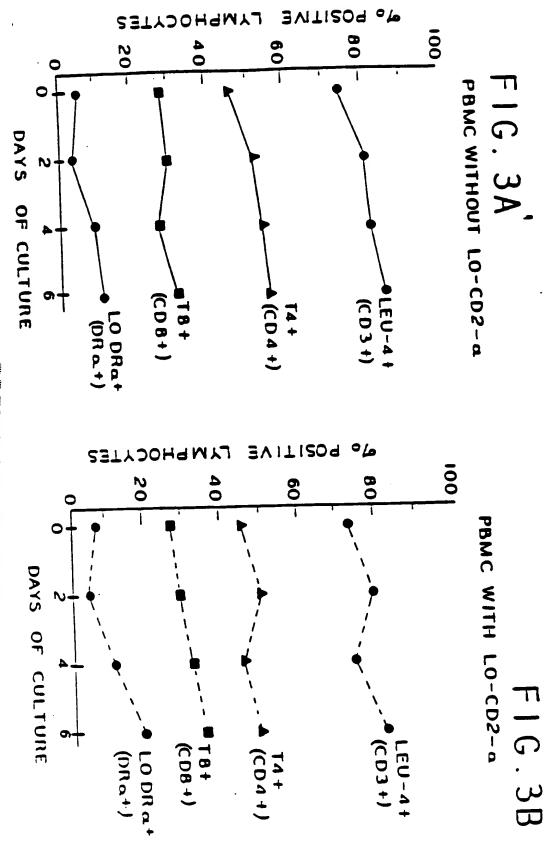
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17/2



DAYS OF CULTURE

F16.4

Effects of LO-CD2a on Resting Cells during MLC

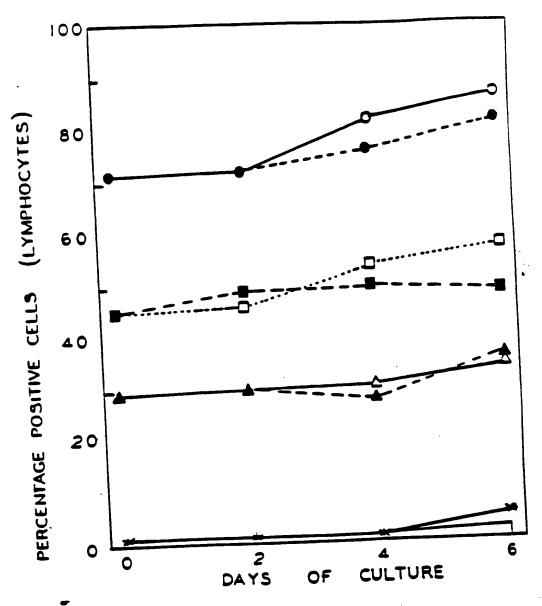
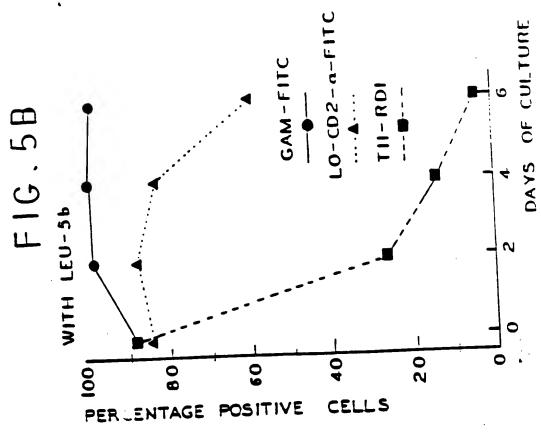
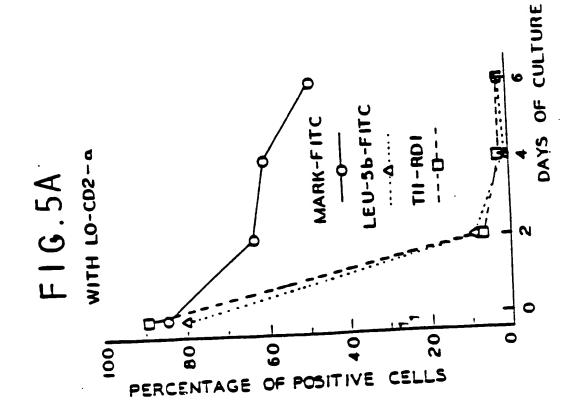
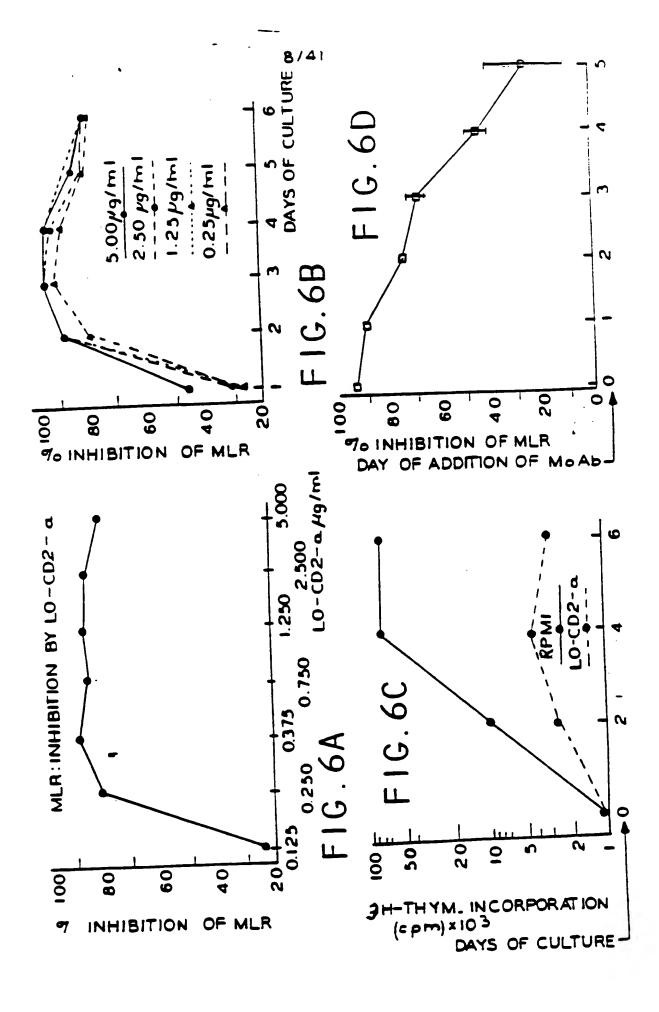


FIG. 8A







MLC: LEU-56+ (CD2+) CELLS

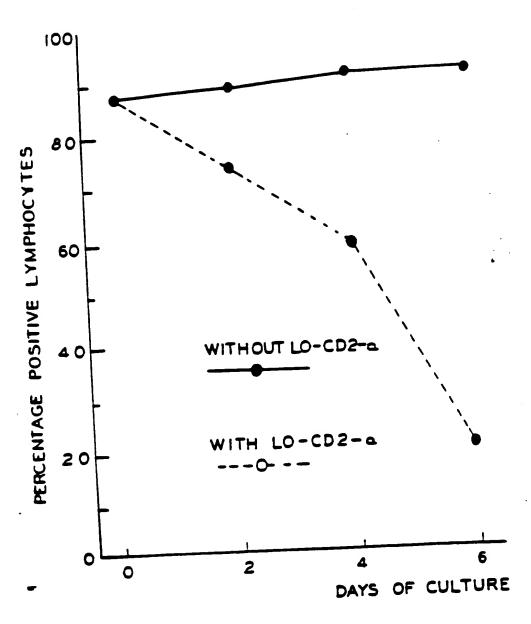
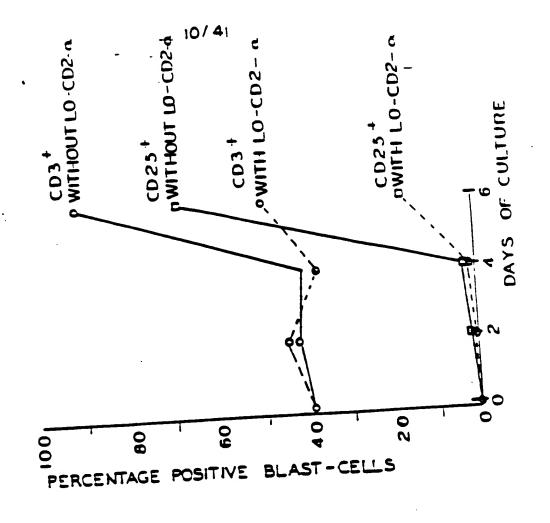
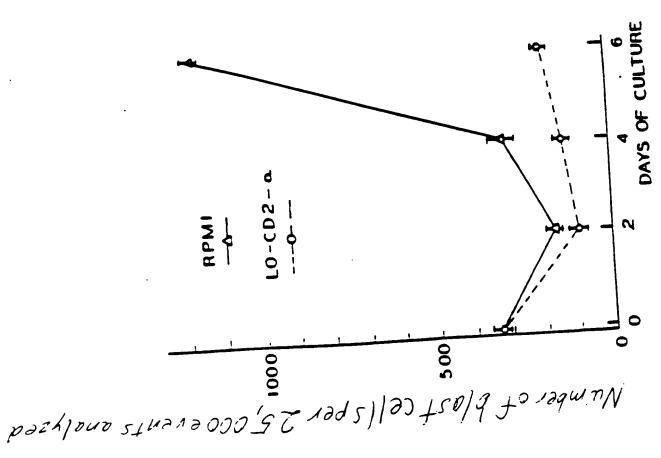


FIG.8B



F16.7

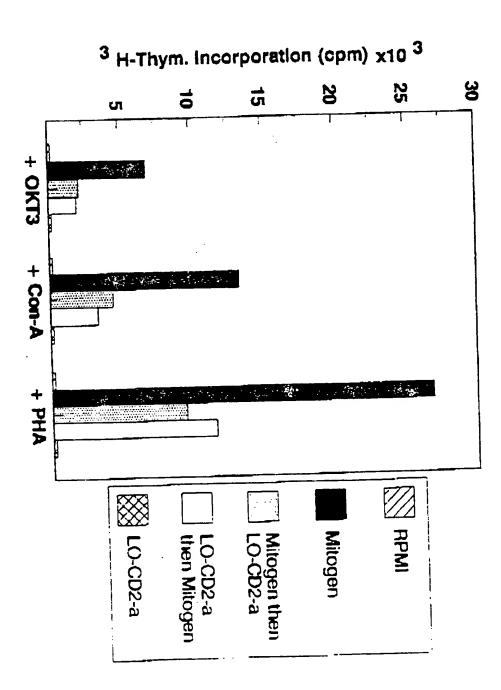


10:15

03 01 93



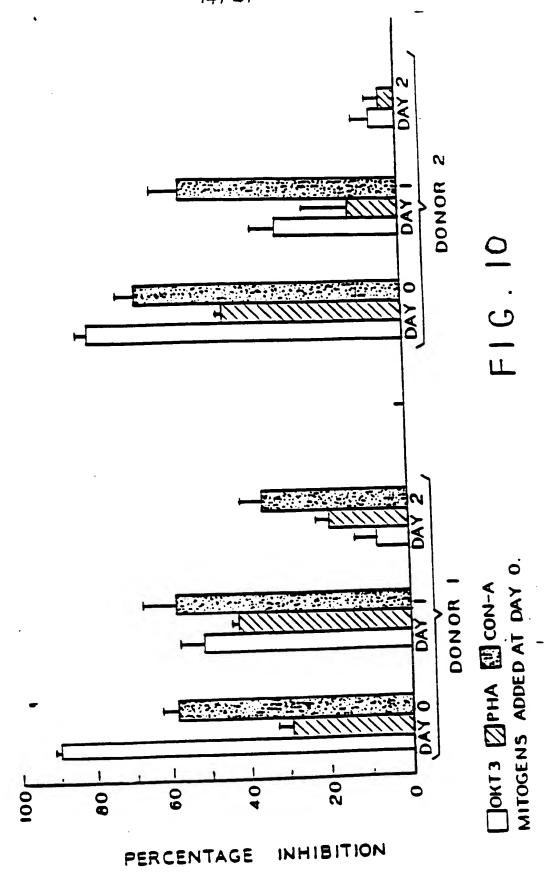
Effects of LO-CD2-a on mitogen-stimulated PBMC

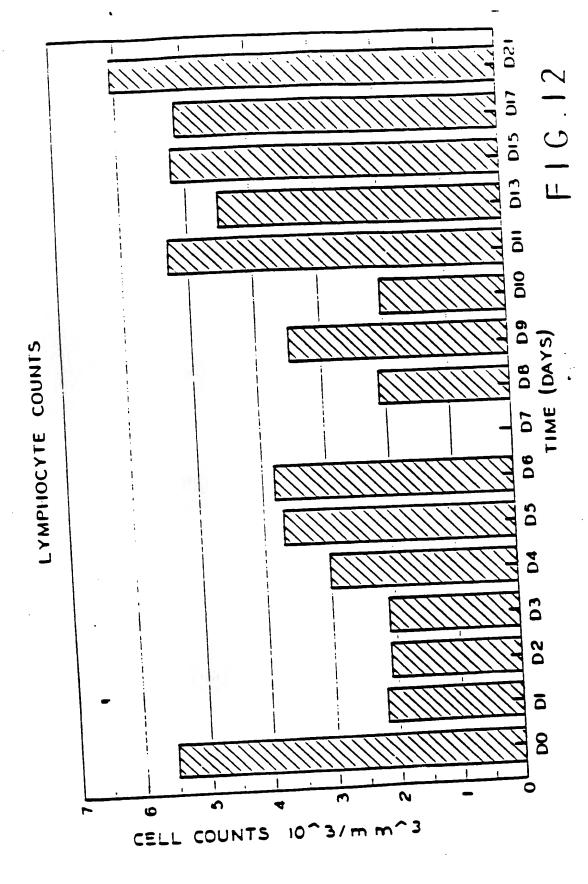


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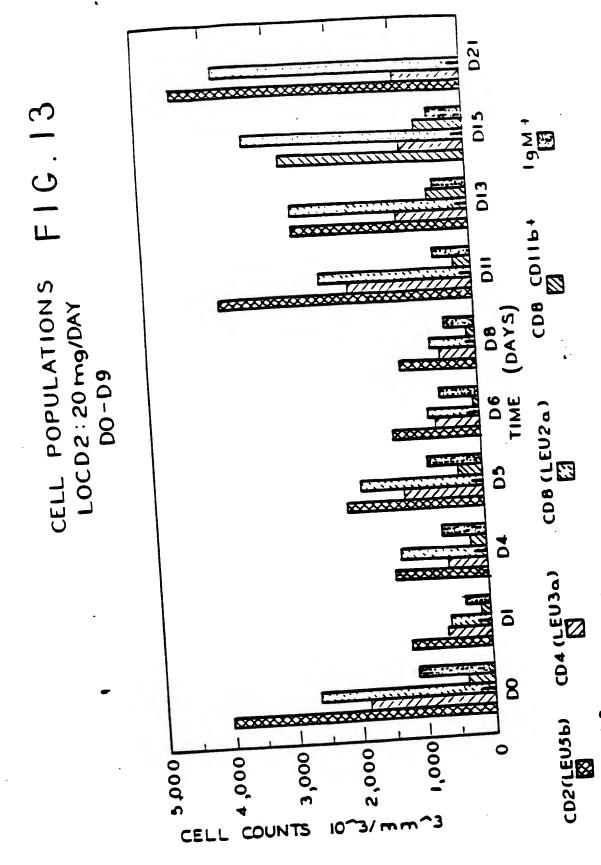
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DOCUMENT. D4DVOS

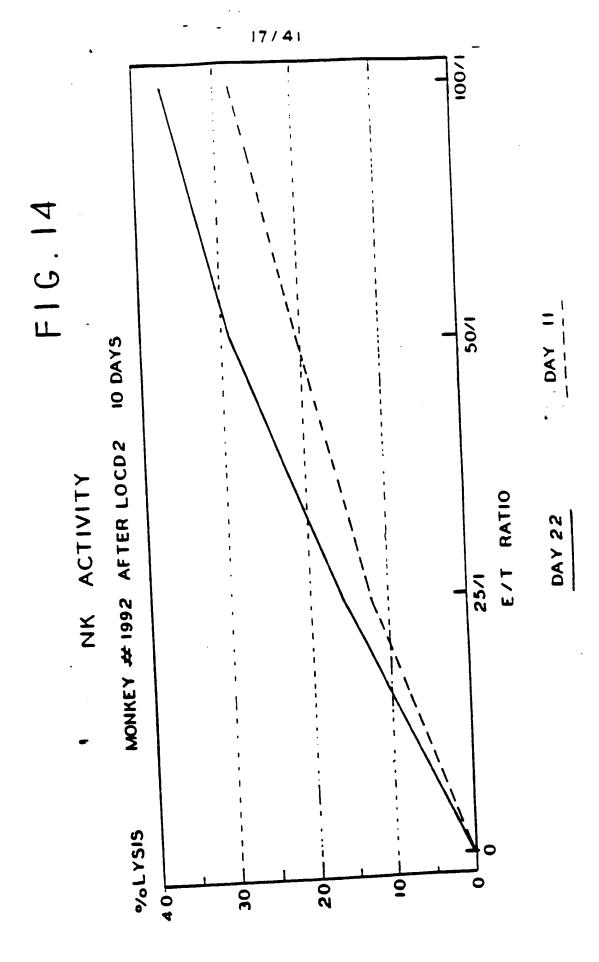


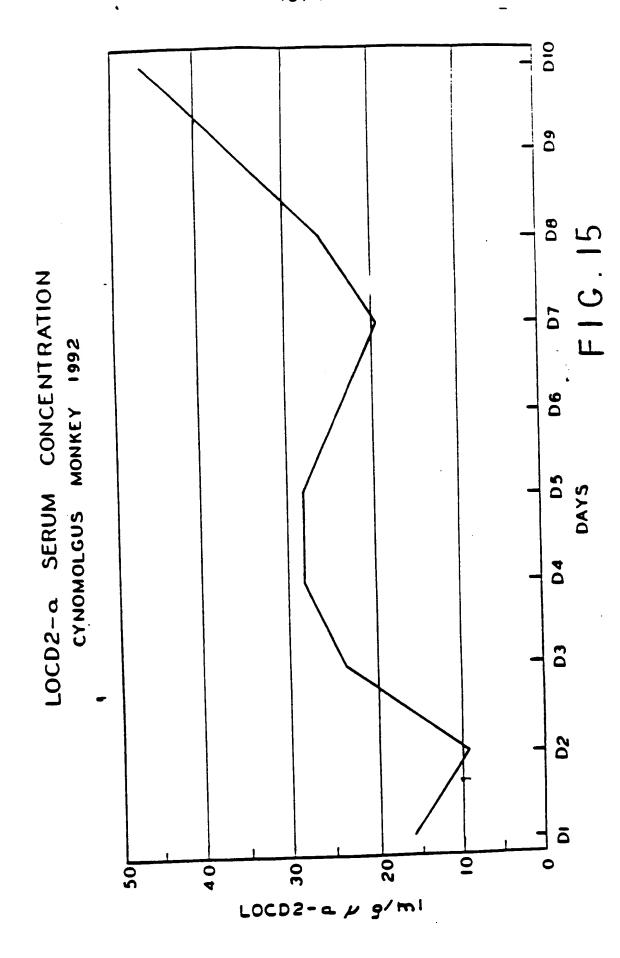


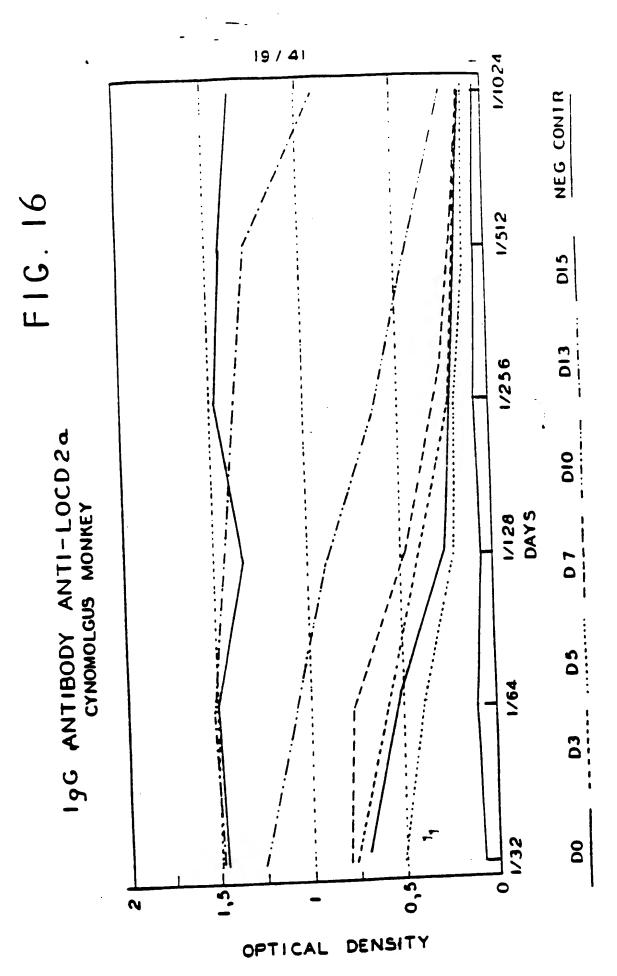
LOCD2 20mg/DAY. DO-D9

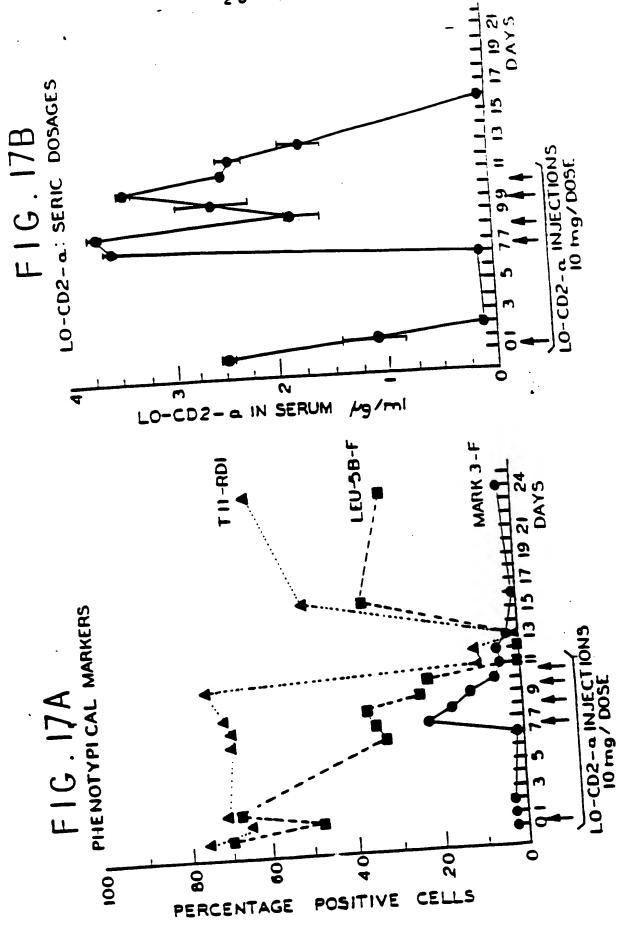


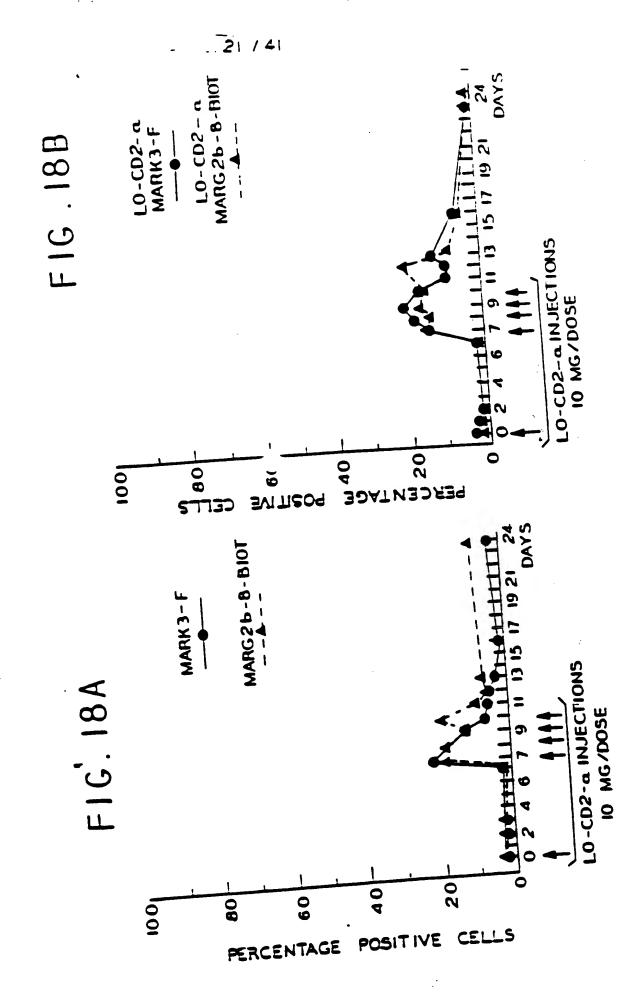
19M+: B CELLS CD8+CDIIS+: NK CELLS

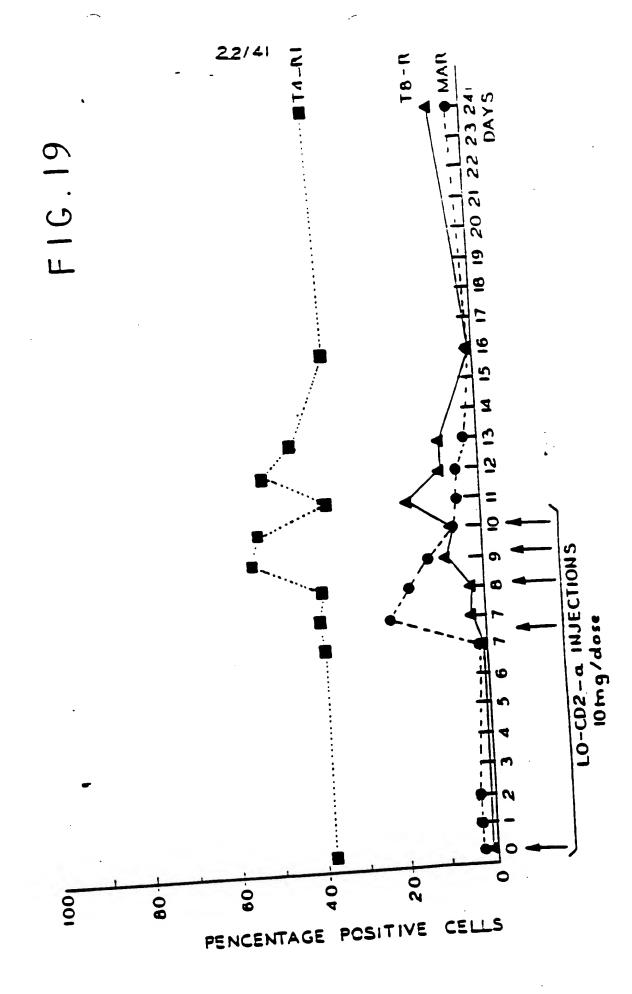


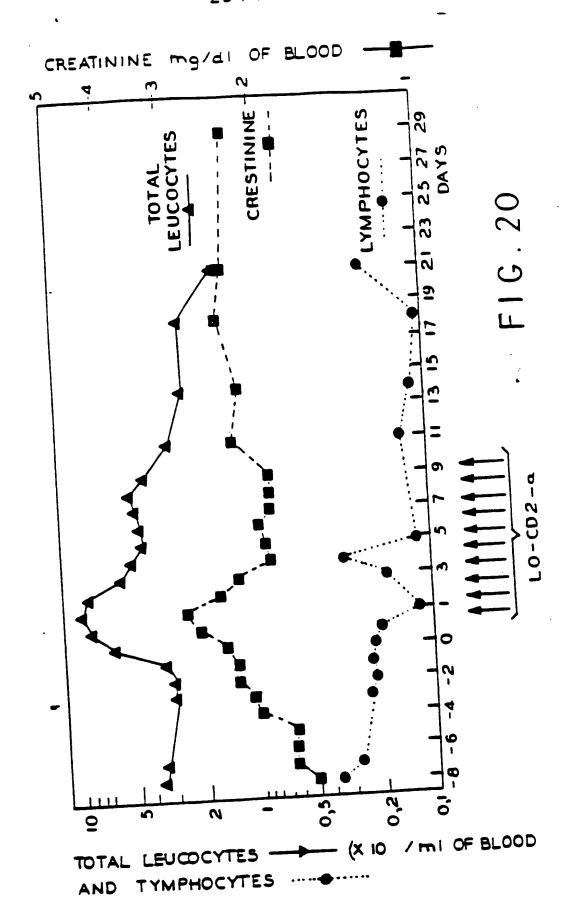


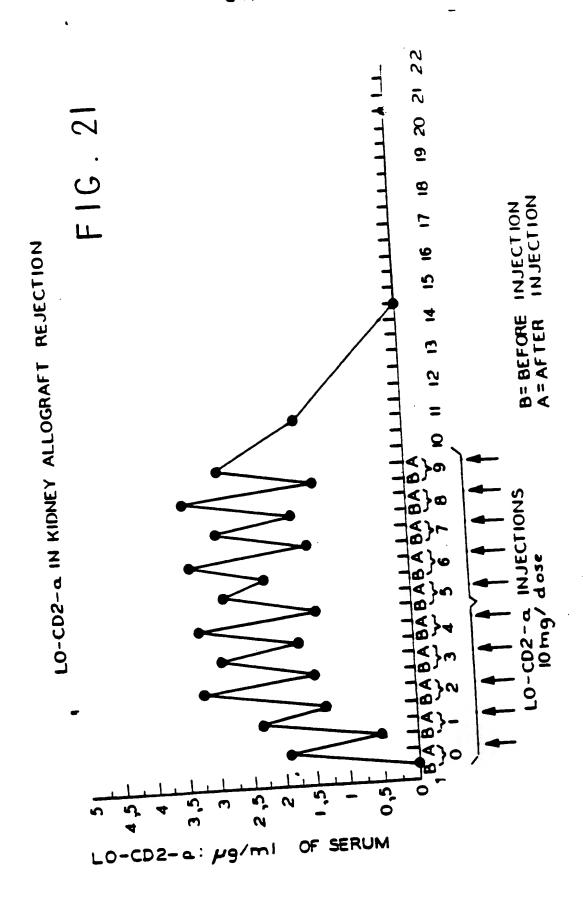




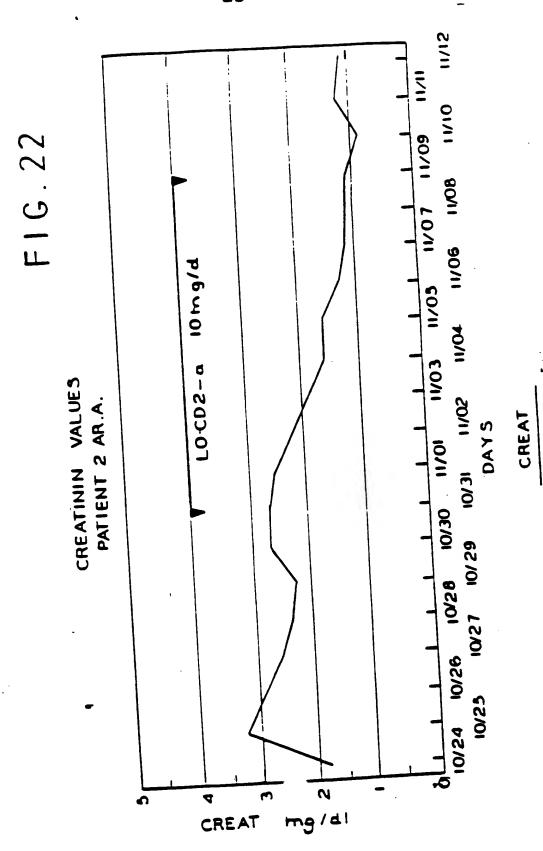


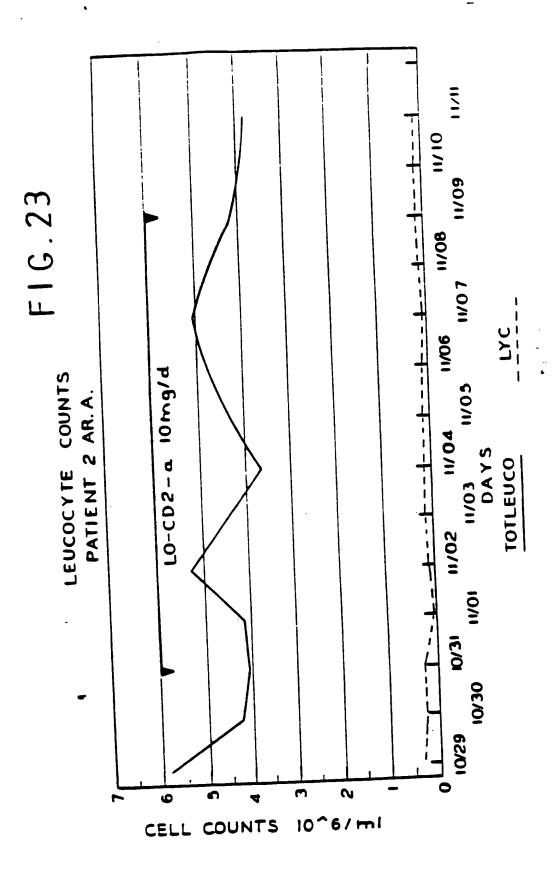


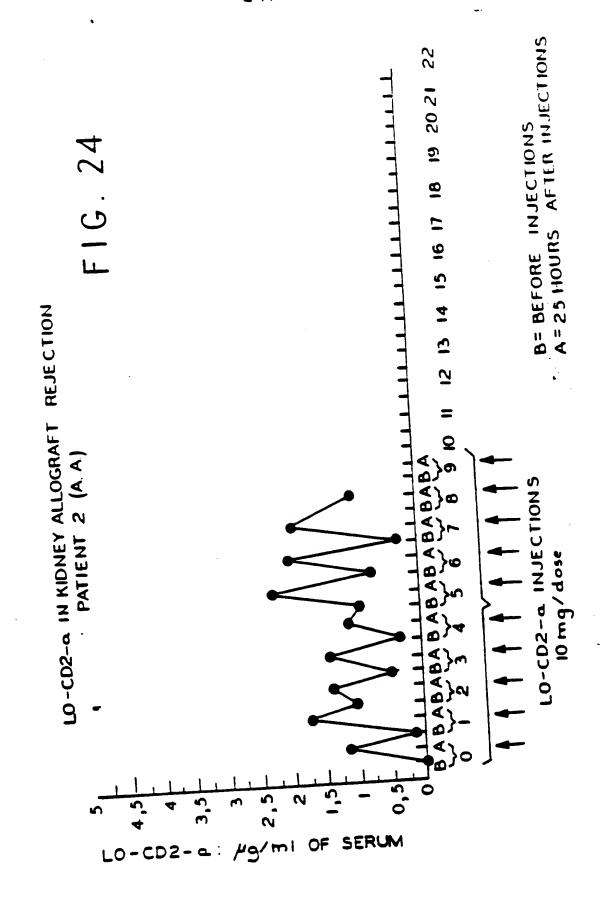


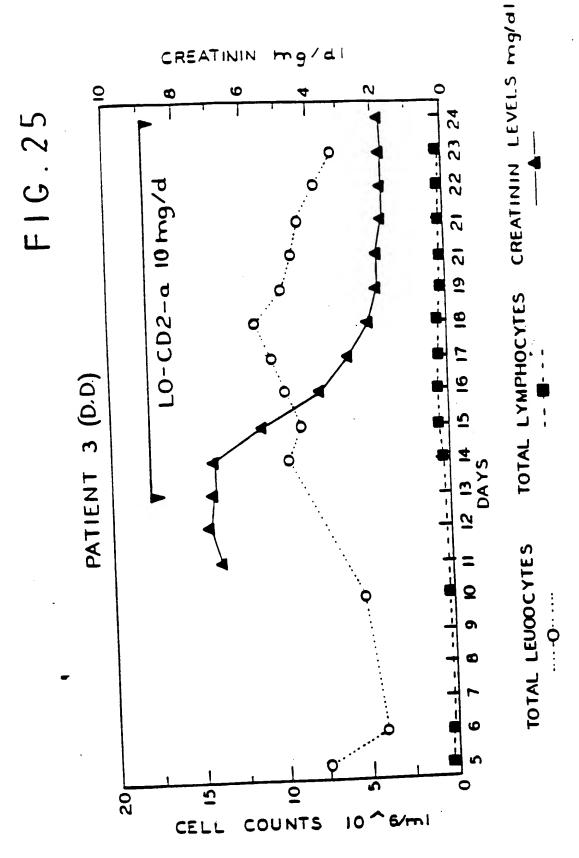


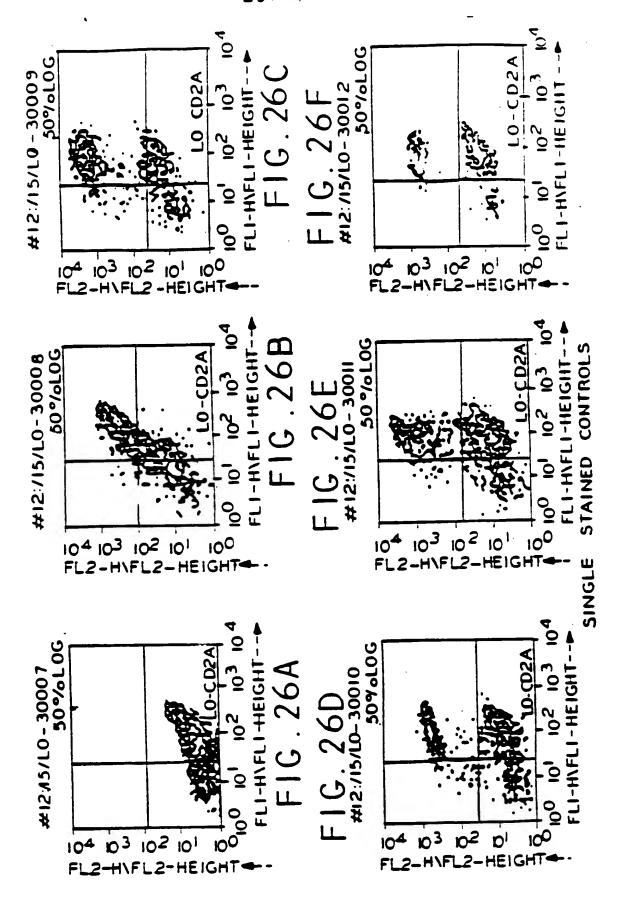
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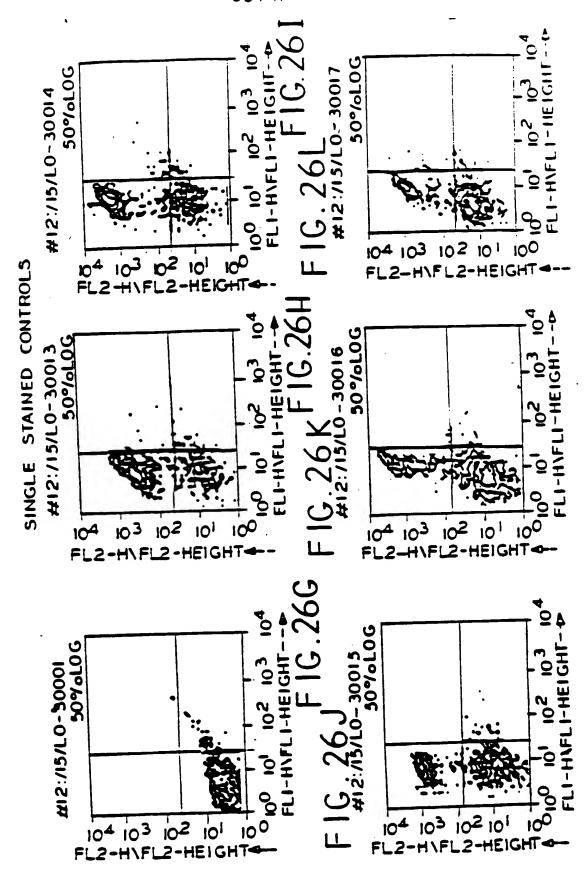


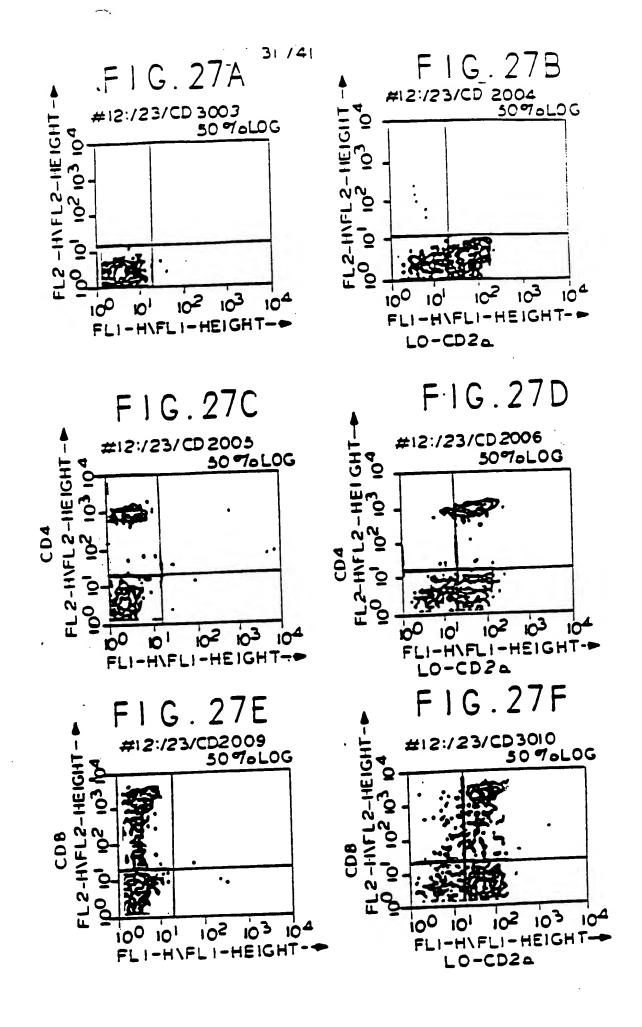


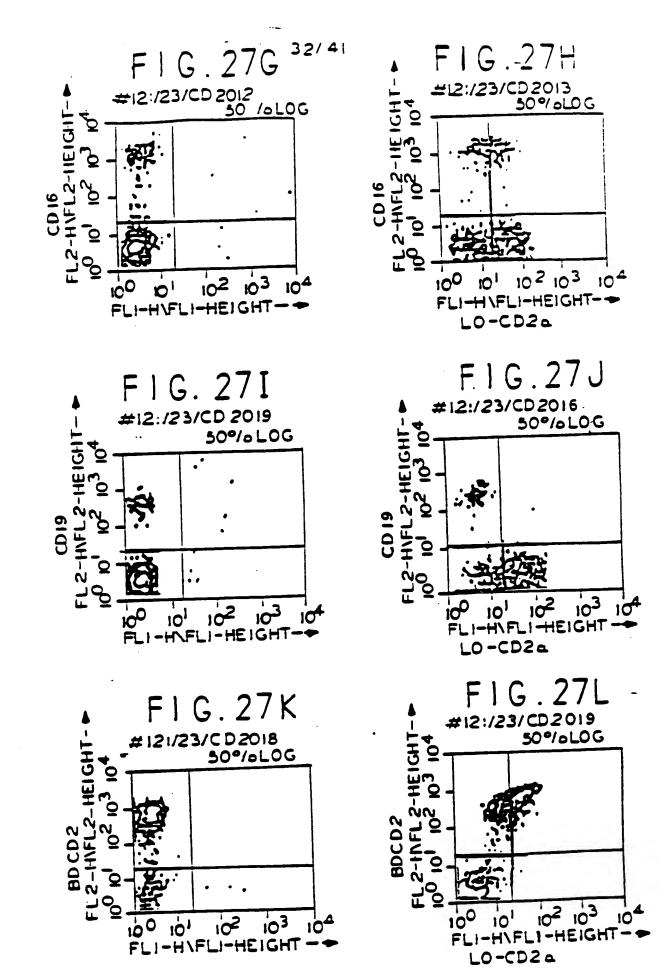


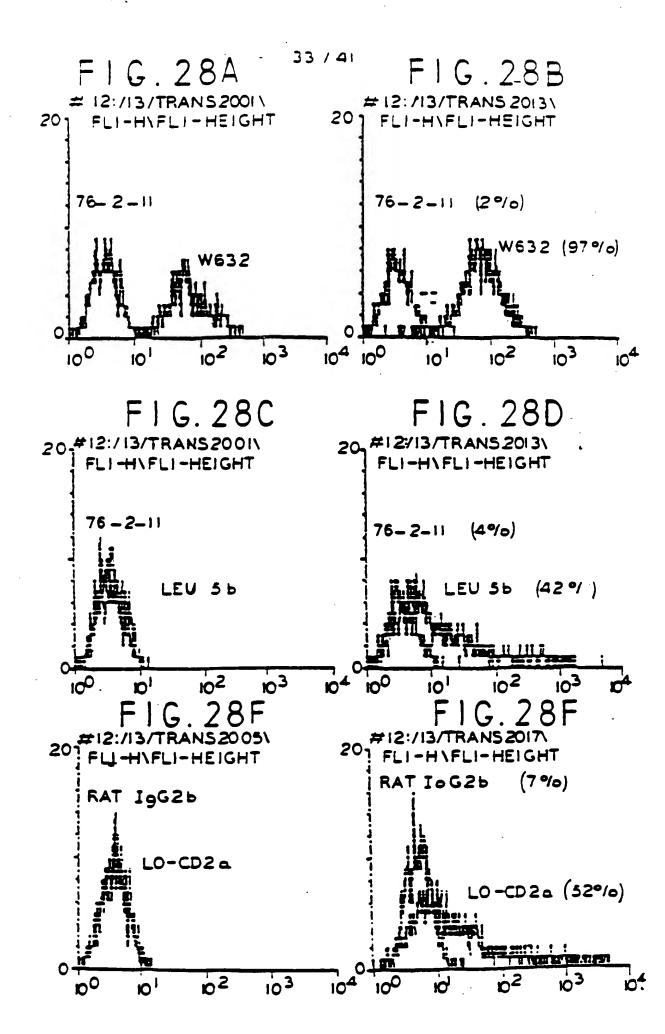












Lo-CD2a VI + Native Leader Sequence

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Seguence Range: 1 to 761
                                                                                                                                                                                                                                                                                                                               ATGATGAGTCCTGTCCAGTCCCTGTTTCTGTTATTGCTTTGGATTCTGGGTAAGTAGAGAATGAGTTACAGGACAAGAATGGGGATGAGATGAGTTCT
                                                                                                                                                                                                                                                                             GACTGCCCATGTTGGCTGTCCATGTGTGGTAAGGCAGGTCCTATTTTCTAAGATGGACACTTGAGATTCCATTACTTGATAATGAGAAATTACAGATGAG
                                                                                                                                                                                                                                      ATAGGATTTGTGCTAAGAGGATTCTAATGTAGATGAGAAGGTGTATGCCATTTAGGATCTGCAACCGAATTGTTTTGTGAAAAAGCATTTGGTATATTTT
                                                                                                                                                                                              {\tt TTAAAAATCACAAAACACCGGGATCTCACAGGAAATGAGTAACAAAAAGTAATTCACAAAGATTGGTTGCAAATTTTTGCACATAACTTTTGTTCTGATC
                                                                                                                                    AGTCAGAGTCTCTTACATAGTAGTGGAAACACCTATTTAAATTIGGTTACCTACAGAGGACAGGCCAATCTCCACAGCCGCTAAITTTAITTIGGTATCCAAAC
S Q S L L H S S G N T Y L N W L L Q R T' G Q S P Q P L I Y L V S K>
                                     TGGAATCTGGGGGTCCCCAACAGGTTCAGTGGCAGTGGGGTCAGGAACAAATTACACTCAAAATCAGTGGAGTGGAAGCTGAGGATTTGGGGGGTTTATTA LESGVPNRFSG78GSGTDFTLK18SGVEAEDLGVYY18CLESGVPNRFSG78GSGTDFTLK18C
  CTGCATGCAATTTACCCATTATCCGTACACGTTTGGAGCTGGGACCAAGCTGGAACTGAAA
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F.GAGTKLELK>
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F19-27

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Sequence Range: 1 to 491
                                                                                                                                                                                                                                                                                 M K C R W I I L F L M A V A T G>
                                                                                                                                                                                                                                                                                                               ATGAAATGCAGGTGGATCATCCTCTTCTTGATGGCAGTAGCTACAGGTAAGGCACTCCCAAGTCCTAAACTTGAGAGATCATACACTTGGGAGACAGTGA
                                                                                                                                                                                                                                         CACTATCTTTGGATTTCTTTCAACAGGGGTCAACTCAGAAGTCCAGCTGCAGCAATCTGGGCCTGAGCTTCAGAGACCCGGGGCCTCAGTCAAGTTGTCG
                                                                                           TGAGGACACAGCAACCTATTTTTGTGCTAGGGGAAAATTCAACTATCGATTTGCTTACTGGGGCCAAGGCACCCTCGTCACAGTCTCCTCA
                                                                  GSIDYVEKFKKATLTADTSSNTAN MQL
                                                                                                                                                                                                210
                                                                                                                                           TEYYMYWVKQRPKQGLELVGRIDPE>
                                                                                                                                                                                                230
GKFNYRF
                                                     440
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F1/me 30

5/17/95

Light Chain Variable Region Sequence of rat LO-CD2a, human HUM5400, and humanized LO-CD2a

Rat LO-CD2a Vk	FR 1 DVVLTQTPPT LLATIGQSV MSSV-LPA	ISCRSEQUEL HS		
Humanized Vk Human HUM5400 Vk	MS-LS -PV-LPA	V Y-	DH FQPR	
Rat LO-CD2a Vk Humanized Vk Human HUM5400 Vk	CDR 2 *60 7 PLIYLVSKLE SGVPNRFSG RKNRDD	S GSGTDFTLKI SG		
Rat LO-CD2a Vk Humanized Vk Human HUM5400 Vk	FR 4 110 YTPGAGTKLE LK Q I-			31

Humanized LO-CD2a Light Chain V Region

Sequence Range: 1 to 807

100	3AT 200	TAC 300	GGT 400	TGT 500	TTG C> 600	* T.* V.>	700 GGG G>	800 *
<u>.</u>	CTGTTTCTGTTATTGCTTTGGATAGTAGAATGAGAATGAGTTACAGGACAAGAATGGGGATGGAGGAT L F L L L W I L G> 1	GTGGTAAGGCAGGTCCTATTTTCTAAGATGGACACTTGAGATTTCCATTACTTGATAATGAGAATTAC 240 250 260 270 280 290 300	TAATGTAGATGAGGTGTATGCCATTTAGGATCTGCAACCGAATTGTTTTGTGAAAAAGCATTTGGT 340 350 360 370 380 390 400	ATATTTTTAAAAATCACAAAACACCGGGATCTCACAGGAAATGAGTAACAAAAGATTGTTTGCATTGCACATAACTTTGT 410 420 430 440 450 460 470 480 500	TCTGATCTATTATAATTTCAGGAACCAATGGTGATGTTGTGATGACCCAGAGTCCACCTTCATTATTGGTAACCTTGGGACAACCAGCTTCCATCTTTTG T N G D V V M T Q S P S L L V T L G Q P A S I S C 1	rttggta L V>	610 620 630 650 660 670 680 700 700 700 700 700 700 700 700 700 7	800 * *********************************
	SGATG	IGAGA)	AAGCA	CATAA 0	TCCA:	TTTA: I Y	0 * GGATC D	Ę
06	ATGGG	ATAAT 290	GAAAA 390	TGCAC	AGCTT A 590	CTAA	690 * CTGAG	790 * \CTTTG
*	AAGA	CTTG	TTGT	ATTT	AACC Q P	AGCCG	3GAAG E	* FTAAP
80	180	280	rrcrr	TGCAA	GGGAC G 580	CCAC	680 * GAGTC G V	780 * GAAT
*	FTACA *	ATTCC	CGAA1	TGGT	CCTT	ATCT	* AGTG	* AGTA
70	ATGAG 170	TTGAG	GCAAC	AAGAT 470	GGTAA V 570	SGCCA.	670 * AAATC K I	770 * ACGTG >
	AGAA	CACT	ATCTG	CACAP	TATT	GCCAC	CTCA	, 7 TCAAA I K>
0.4	AGTAC	ATGG	TAGG/	AATT	TCAT	AGAG	SO * CCACA	SO SGAAA E
09	GGTAA G>	TAAGA'	CATTT	AAGTA	CACCTT P P 5	3CTAC	660 * * 3ATTTC D F	760 * * * AGCTGG K L
*	TCTG	TTTC	ratgo	ACAA	AGTC(S 1	GGTTK W L	AACAC	ACCA
\$	NGGAT W 1		GGTC:	AGTA	CCAG	AATT	650 * GTGG/ S G	750 * vAGGG
*	GCTT	AGGT	AGAA	AATG	ATGACO M T	ATTTA Y L	4GGGA	* 3GACA G Q
40	L L L	AAGGC 240	AGATG 340	CAGGA	IGTG#	ACCT/	640 * GCTC2 G S	740 GTTTC
	rctrg1	TGGTV	ATGT	CTCA	ATGT D V	AAAC	+ :AGTG S	* FACAC Y T
0 *	CTGTT L F	ATGTG	TTCTA	GGGAT	regre G	osu * TAGTGG/ S G	630 * AGGTTC R F	730 * ATCCG1 Y P
30		TCCA		SACCG	CCAAT F N	TAGTV	* 6. GACAC D	7. ATTA H
*	rccac	, GGCTÇ	TAAGI	AACA(GGAA	TACA L H	d .	Accc
20	AAGCTTCATGATGAGTCCTGTCCAGTCC M M S P V Q S 110 120 1	GAGTTCTGACTGCCCATGTTGGCTGTCC	AGATGAGATAGGATTTGTGCTAAGAGGA	ACAN 420	mttca	S10 S20 S20 S20 S30 S30 S30 S30 S30 S30 S30 S30 S30 S3	610 620 * * * * AACTGGAATCTGGGGTCCCC	1 710 720 730 740 750 760 770 780 790 790 790 790 790 790 790 790 790 79
•	GAGT	• CCCA	ATTT	AATC	TAAT	AGAGT	ATCTC S	ATGC
10	ATGAT	GACTG	* SATAGG 310	TTAA 410	TATE	510 * * * STCAAGTCAG S S Q	610 Tregal	710 * ACTGC
	TTCA	TCTC	rgagi	TTTT.	GATC'	GTCA	AAAC K	j * 'ATTA '
,	AAGC	GAG	AGA'	ATA	TCT	CAG R	TCC	, TTT V

TGGATCC

F1932

Heavy Chain Variable Region Sequences frat LO-CD2a, human Amu 5-3, and humanized LO-CD2a

		FR 1			FR 2	
Rat LO-CD2a Vh	: 10 EVQLQQSGPE	LORPGASVKL	SCKASGYIFT	EYYMYWYXQR	PKQGLELVGR	
Humanized Vh Human Amu 5-3 Vh	6y-	AKKA	T	GR-A	-GWX	
Rat LO-CD2a Vh Humanized Vh Human Amu 5-3 Vh		VEKFKKKATL	TADTSSNTAY	-RD-	TATYFCARGE	
Rat LO-CD2a Vh Humanized Vh Human Amu 5-3 Vh	/////-	FR 4			Fig.	33

Sequence Range: 1 to 701

AAGCTTCATGAAATGCAGGTGGATCATTCTTGATGGCAGTACGTAAGGCACTCCCAAGTCCTAAACTTGAGAGATCATACACTTGGGAG M K C R W I L F L M A V A T G 110 120 130 140 150 160 170 180 190 200 ACAGTGACACTATTGGATTTCTTTCAACAGGGGTCAAGGTGAGGTGAAGAAGCCTGGGGCTCAGTGGAA ACAGTGACACTATCTTTGGATTTCTTTCAACAGGGGTCAACGTCAGGTGAGGTGAAGAAGCCTGGGGCTCAGTGGAA ACAGTGACACTATCTTTCAACAGGGGTCAACTCACAGGTGAGGTGAAGAAGGCTGAGGGCTGAGGGCTGAGGAGGCTCAGTGGAA ACAGTGACACTATCTTTCAACAGGGGTCAACACTCACAGGTGAGGACTGAGGGCTGAGGGCTTGAGGTTGAGTGGAAGGATCGAT A S G Y T F T E Y Y M Y W V R Q A P G Q G L E L M G R I D A S C K A S G Y T F T E Y Y M Y W V R Q A P G Q G L E L M G R I D A S C CTGAAGGCGTAGTTTAAGAAAAAGGTCACCTGACAGGCCTTAAGGACTGAGGCTAATGGAGCTGAGGCCCTAAGGACGCTAATGAGACTGAGGCCTAAGGACGCTAATGAAAAAAGGTCACCTGACGCTAAATGGACTGAGGCCTAAATGGACTGAGGCCTAATGGACTGAGGCCTAAATGGACTGAGCCCTAAGGACGCTAATTAAGAAAAAAAA	CATCCTCTT 130 130 TTTCAACAG CACCTTCAC T F T 330 A F T CT F CT F	CTTGATGGCA(L M A 140 AGGTCAACTC) V N S 240 CGAGTACTAT 340 TTTAAGGAAA	rctcttcttgatggcagtagctaaggcactcccaagtcctaaacttgagagatcatacattgggag 130 140 150 160 170 180 190 200 130 140 150 160 170 180 190 200 130 240 250 260 270 280 290 300 130 240 250 260 270 280 290 300 140 350 360 370 380 390 400	SCTAAGGCACTC G> 160 * 160 L V Q S 260 * 260 * 360 V R Q A GACCGCTGACI	CCCAAGTCCT 170 170 S G A E 270 A CCCTGGACA? CCCTGGACA?	TAAACTTGAGAAGE V K K K K K K K K K K K K K K K K K K	AGATCATACA 190 AGCCTGGGGC P G A 290 * * * * * * * * * * * * * * * * * *	CTTGGGAG 200 STCAGTGAA S V K 300 A AGGATGAT R I D>
GACACTATCTTTGGATTTC 210 220 CCTGCAAGGCTTCTGGATA S C K A S G Y 310 320 AGACGGTAGTATTGATTAT CD G S I D Y	130 TITICAACAG 230 CACCITICAC T F T 330 CITICAGAAG CITICAGAAG	140 CGGTCAACTC V N S 240 CGAGTACTAT CGAGTACTAT TTTAAGAAAA	150 350 350 350 350	160 TGGTGCAGT L V Q 260 * * * TGCGACAGGC ' R Q A 360	170 CTGGGGCTG; S G A 270 * 270 P G Q 370 * 370	180 AGGTGAAGAA E V K K 280 AGGGCTTGAG G L E	190 AGCCTGGGGCC (P G A 290 * * * SCTGATGGAA L M G	200 CTCAGTGAA S V K 300 AGGATCGAT R I D>
CCTGCAAGCTTTCGATTTC 210 220 CCTGCAAGCTTCTGGATA S C K A S G Y 310 310 320 AGACGTAGTATTGATTAT S D G S I D Y	TTTCAACAG 230 CACCTTCAC T F T 330 CTTGAGAAG V E K	GGGTCAACTC V N S 240 CGAGTACTAT CGAGTACTAT 340 TTTTAAGAAAA	ACAGGTGCAGG O V Q 250 ATGTACTGGGT M Y W V 350 AGGTCACCCTX	TGGTGCAGT L V Q 260 GCGACAGGC GCGACAGGC A R Q A 360 A SACCGCTGAC	CTGGGGCTG S G A] 270 CCCTGGACA P G Q 370	AGGTGAAGAA E V K K 280 AGGGCTTGAG G L E	AGCCTGGGGCC P G A 290 **CTGATGGAA L M G 390	CTCAGTGAA S V K 300 AGGATGAT R I D>
210 220 rccrccaacctrcrccara s c k a s G Y 310 320 AAGACGTAGTATTAT	230 ACACCTTCAC T F T 330 ACTTGAGAAG V E K	240 CGAGTACTAT E Y Y 340 TTTAAGAAAA	250 TATGTACTGGG1 M Y W V 350	260 rgcgacaggc / R Q A 360	270 CCCTGGACA P G Q 370	280 * * * AGGGCTTGAG G L E	290 * * * scrgargggaa L M G	300 AGGATCGAT R I D>
TCCTGCAAGGCTTCTGGATA S C K A S G Y 310 320 AAGACGTAGTATTGATTAT E D G S I D Y	CACCTTCAC TFT 330 CTTGAGAAG CGTTGAGAAG	CGAGTACTAT E Y Y 340 TTTAAGAAAA	PATGTACTGGGT M Y W \ 350 AGGTCACCCTX	rGCGACAGGC / R Q A 360 * *	CCCTGGACA) PGQQ 370 AGGTCCTCT	AGGCCTTGAG G L E 380	SCTGATGGGAA L M G 390	AGGATCGAT R I D>
310 320 * AGACGCTAGTATTGATTAT EDGSIDY	330 * * * CTTCAGAAG V E K	340 TTTAAGAAAA	350 * AAGGTCACCCTV	360 * 3ACCGCTGAC	370 * * * ACGTCCTCT	380	390	400
AAGACGGTAGTATTGATTAT E D G S I D Y	IGTTGAGAAG V E K	TTTAAGAAAA	AAGGTCACCCTK	SACCGCTGAC	ACGTCCTCT) #))	*	*
		F K	K V T L	T A D	T S S	AGCACAGCCT S T A	racatggagct Y M E L	rgagcagcc L S S>
410 420	430	440	450	460	470	480	490	200
TGACCTCTGACGACACGCCGTGTATTACTGTGCGAGAAAGTTTAACTATAGGTTTGCTTACTGGGGCCAAGGAACCCTGGTCACGTCTCCTCAGG	rattactgtg Y Y C	CGAGAGGAAA A R G K	AGTTTAACTATA K F N Y	AGGTTTTGCTT R F A	ACTGGGGCC.	AAGGAACCCT Q G T I	RGGTCACCGTC	CTCCTCAGG S S>
510 520	530	540	550	\$ \$	570	\$ 580	\$ \$	* * *
TGAGTCCTTACAACCTCTCTTCTATTCAGCTTAAATAGATTTTACTGCATTTGTTGGGGGGGAAATGTGTATCTGAATTTTCAGGTCATGAAGGACT	CTATTCAGCT	TAAATAGATT	ITTACTGCATT	rerreceeed	GAAATGTGT	GTATCTGAA	rttcaggtcai	IGAA GGACT
610 620	630	640	650	099	670	¢ * *	069	700
A CASA NA CASA SA PASA SA PASA SA PASA SA CASA CA	SCOTO A TITLE	Jese Contract	TRATICAGACI	AGACATCCTC	AGCTCCCGG	ACTTCATGG	CAGAGATTTA	ATAGGGATC

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Binding of LO-CD2a and LO-CD2a Hu to Jurkat Cells

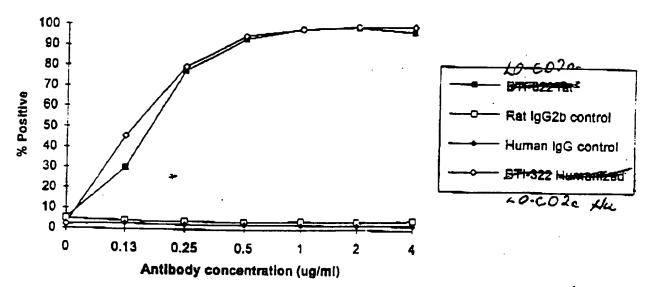
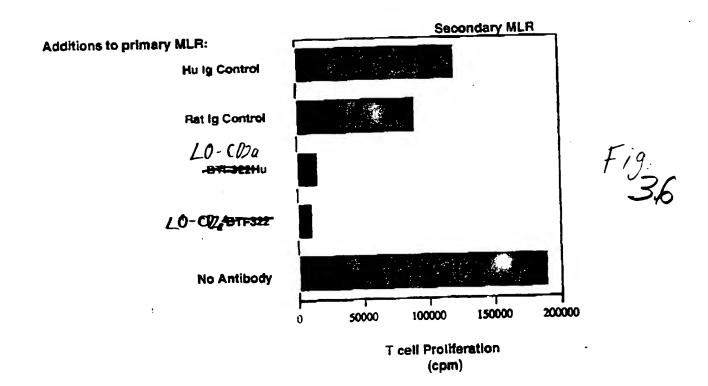
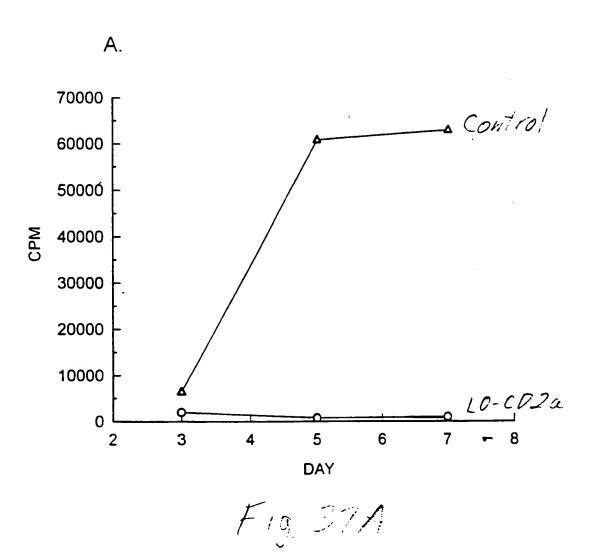
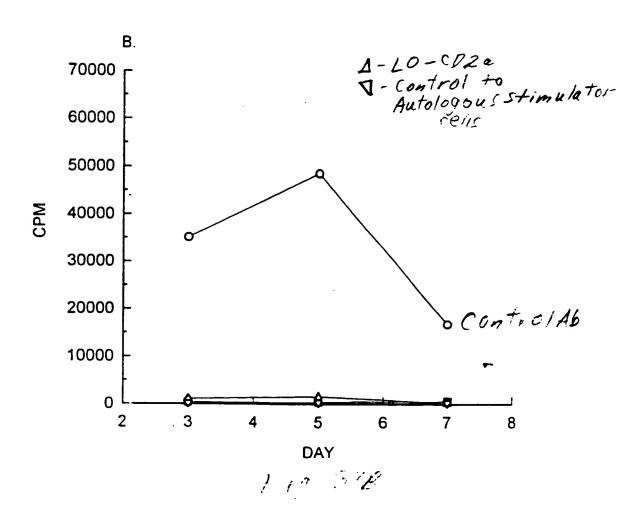


Fig. 35

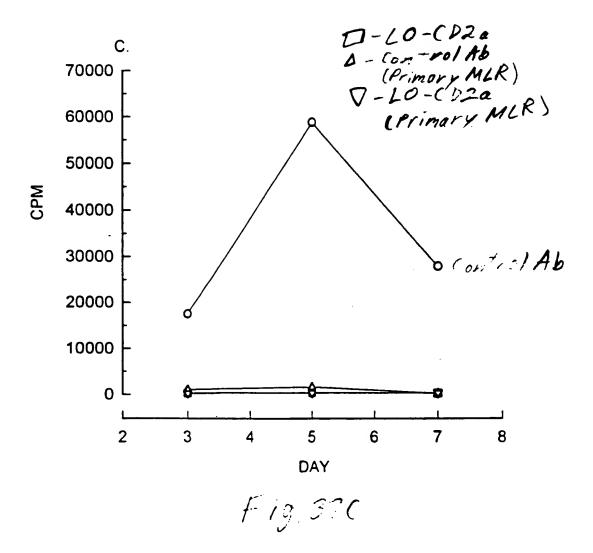
Induction of Hyporesponsivene s in vitro

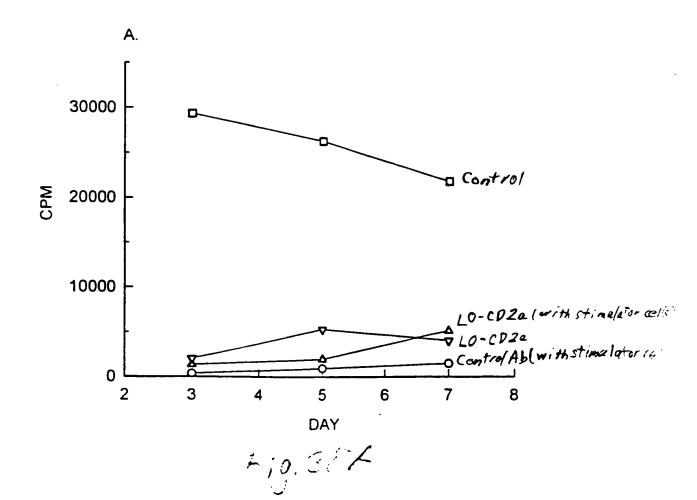


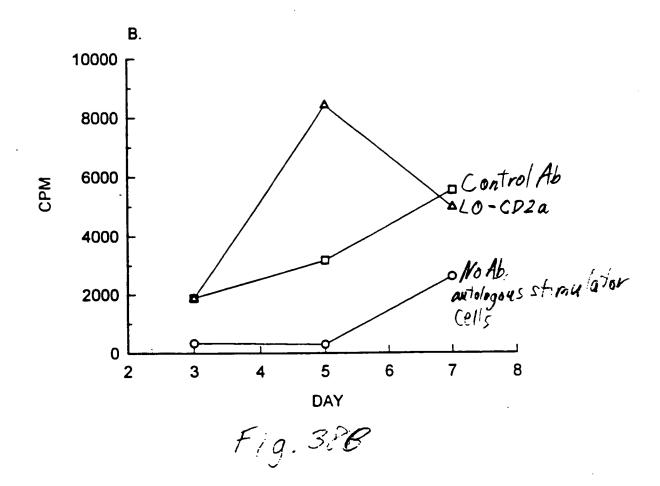


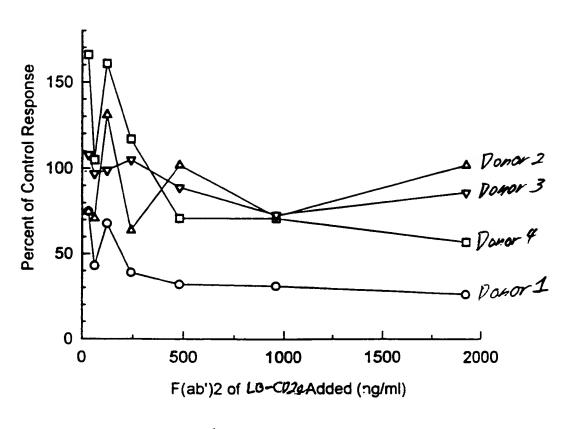


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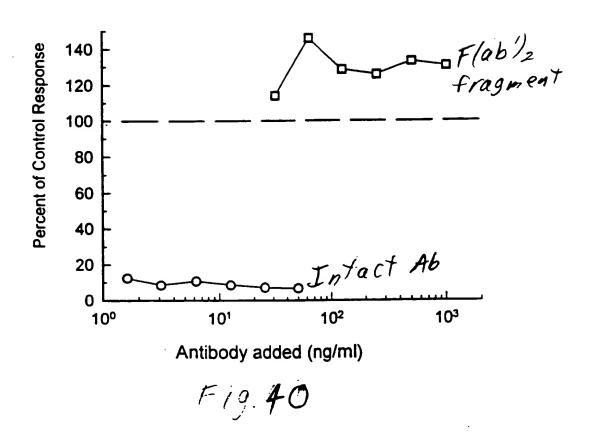




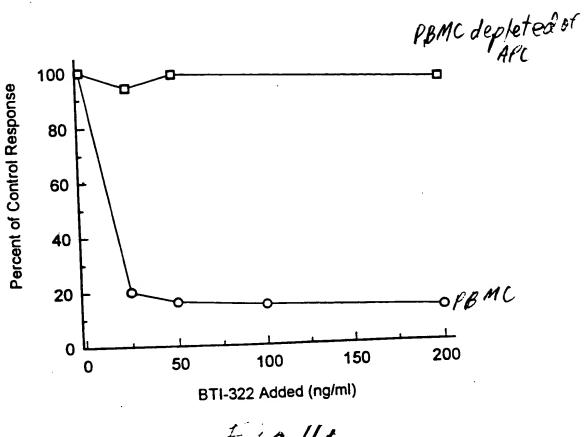




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